REMARKS/ARGUMENTS

The Office Action mailed October 22, 2003 has been carefully reviewed and the foregoing amendments are made in response thereto. In view of the amendments and the following remarks, Applicants respectfully request reconsideration and reexamination of this application and the timely allowance of the pending claims.

Claim 39 has been amended to require that the second nucleic acid sample is reproducibly reduced in complexity relative to the first nucleic acid sample. Support for this amendment may be found in originally filed claim 1. Claim 39 has also been amended to add the limitation that the probes of the array interrogate the genotype of a plurality of polymorphisms. Support for this amendment may be found at page 32 lines 17-25. Claim 39 has been further amended to clarify that a computer system is used to predict polymorphisms present on amplified fragments. Support for this amendment may be found on page 20 lines 24-29. No prohibited new matter has been introduced by these amendments.

In the Office Action, Claims 39-53 have been rejected under 35 U.S.C. §103(a) over McCaskey-Feazel et al. (U.S. Patent No. 6,100,030, issued August 8,2000, priority January 10, 1997) in view of DeRisi et al. (Science, October 1997, vol. 278, pages 680-686) and Moyer et al. (Applied and Environmental Microbiology, July 1996, vol. 62, no. 7, pages 2501-2507).

Amended claim 39 provides a method for genotyping a plurality of polymorphisms using an array of probes. The array of probes is designed to interrogate a set of polymorphisms that have been selected because they are predicted by a computer system to be present on fragments that are predicted by a computer system to be present in a sample that has been fragmented and amplified by a selected, predetermined method.

Moyer et al. is cited as disclosing a method of employing a computer simulation to predict fragmented nucleic acid sequences. Moyer et al. does not teach the use of a computer system to predict the fragments and polymorphisms that will be present in a sample after fragmentation by a selected method and amplification by a selected method as required by amended claim 39. Moyer et al. also fails to teach the design of an array to interrogate the polymorphisms predicted to be present after fragmentation by a selected

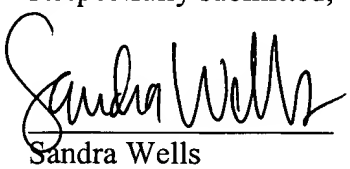
method and amplification by a selected method. As stated in the Office Action McCasky Feazel et al. do not teach the use of a computer system to predict fragments. McCasky Feazel et al. also fails to teach or suggest that the nucleic acid sample is analyzed by hybridization to an array that is designed to interrogate the genotype of polymorphisms on fragments in a reduced complexity sample where the complexity of the sample is reduced by a method that reproducibly results in the amplification of polymorphism containing fragments identified by a computer. Reconsideration and withdrawal of the rejection of claims 39-53 is respectfully requested.

CONCLUSION

For the foregoing reasons, Applicants believe all the pending claims are now in condition for allowance and should be passed to issue. Applicants believe that no extension of time is required for submission of this paper. However, if an extension is required, Applicants petition for any necessary extension of time and authorize the Commissioner to deduct any required fees from the undersigned's Deposit Account No. 01-0431. Please deduct any additional fees from, or credit any overpayment to the above-noted Deposit Account. If the Examiner feels that a telephone conference would in any way expedite the prosecution of the application, please do not hesitate to call the undersigned at (408) 731-5768.

Date: 4/20/04

Respectfully submitted,



Sandra Wells
Reg. No. 52,349

Customer No. 22886
Legal Department
Affymetrix, Inc.
3380 Central Expressway
Santa Clara, CA 95051
Tel: 408/731-5768
Fax: 408/731-5392